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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 11:23:16 ; Search time 102 Seconds
(without alignments)

1620.718 Million cell updates/sec

Title: US-10-783-297A-3

Perfect score: 93

Sequence: 1 tgaagcgacccgggtgcc.....tcattctctctctgcagg 93

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	88.2	1001	3	US-09-641-638-320
2	82	88.2	1001	3	US-10-170-097-320
3	82	88.2	26103	3	US-09-949-016-15685
4	82	88.2	26105	3	US-09-949-016-11879
5	36.6	39.4	1899	3	US-09-919-060-15
6	36.6	39.4	1899	3	US-09-919-060-16
7	36.6	39.4	2693	3	US-09-919-060-12
8	36.6	39.4	2693	3	US-09-919-060-14
9	28.4	30.5	601	3	US-09-949-016-54781
10	28.4	30.5	601	3	US-09-949-016-54782
11	28.4	30.5	601	3	US-09-949-016-54783
12	28.4	30.5	24942	3	US-09-949-016-13318
13	28	30.1	1131	3	US-09-902-540-7216
14	28	30.1	4410	3	US-09-902-540-673
15	27.8	29.9	162025	3	US-09-834-700-13
16	27.8	29.9	162025	3	US-09-834-700-14
17	27.8	29.9	162025	3	US-09-834-700-17
18	27.8	29.9	162025	3	US-09-834-700-18
19	27.4	29.5	218	3	US-09-540-236-21
20	27.4	29.5	2531	2	US-08-299-849B-13
21	27.4	29.5	2531	2	US-08-299-849B-14
22	27.4	29.5	2531	2	US-08-142-368A-13
23	27.4	29.5	2531	2	US-08-142-368A-14
24	27.4	29.5	2531	3	US-08-967-727-13

C 25	27.4	29.5	2531	3	US-08-967-727-14	Sequence 14, Appl
C 26	27.4	29.5	2531	3	US-08-037-230D-13	Sequence 13, Appl
C 27	27.4	29.5	2531	3	US-08-037-230D-14	Sequence 14, Appl
C 28	27.4	29.5	2531	3	US-09-583-850-13	Sequence 13, Appl
C 29	27.4	29.5	2531	3	US-09-583-850-14	Sequence 14, Appl
C 30	27.4	29.5	2531	3	US-09-579-197-13	Sequence 13, Appl
C 31	27.4	29.5	2531	3	US-09-579-197-14	Sequence 14, Appl
C 32	27.4	29.5	2531	3	US-09-404-026-13	Sequence 13, Appl
C 33	27.4	29.5	2531	3	US-09-404-026-14	Sequence 14, Appl
C 34	27.4	29.5	2531	3	US-09-312-464-13	Sequence 13, Appl
C 35	27.4	29.5	2531	3	US-09-312-464-14	Sequence 14, Appl
C 36	27.4	29.5	2531	3	US-09-583-848A-13	Sequence 13, Appl
C 37	27.4	29.5	2531	3	US-09-583-848A-14	Sequence 14, Appl
C 38	27.4	29.5	4895	3	US-09-056-105-10	Sequence 10, Appl
C 39	27.4	29.5	11495	3	US-09-056-105-9	Sequence 9, Appl
C 40	27	29.0	1841	3	US-09-050-516-3	Sequence 3, Appl
C 41	27	29.0	1841	3	US-10-278-547-3	Sequence 3, Appl
C 42	27	29.0	2894	3	US-09-050-516-27	Sequence 27, Appl
C 43	27	29.0	2894	3	US-10-278-547-27	Sequence 27, Appl
C 44	26.8	28.8	601	3	US-09-949-016-18615	Sequence 18615, A
C 45	26.8	28.8	601	3	US-09-949-016-134770	Sequence 134770, A

ALIGNMENTS

RESULT 1

US-09-641-638-320
; Sequence 320, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Matta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Amick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 320
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 10-308-116 : polymorphic base C or T
; NAME/KEY: misc binding
; LOCATION: 481..500
; OTHER INFORMATION: 10-308-116.misl, potential
; NAME/KEY: misc binding
; LOCATION: 502..521
; OTHER INFORMATION: 10-308-116.mis2, potential complement
; NAME/KEY: primer bind
; LOCATION: 386..403
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer bind
; LOCATION: 754..771
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc binding
; LOCATION: 489..513
; OTHER INFORMATION: 10-308-116 potential probe

US-09-641-638-320

Query Match 88.2%; Score 82; DB 3; Length 1001;
Best Local Similarity 98.9%; Pred. No. 3.2e-18;
Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60
DB 394 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 453
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAG 93
DB 454 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAG 487

RESULT 2

US-10-170-097-320
Sequence 320, Application US/10170097
Patent No. 6794143

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GEN-T114XC2D1
CURRENT APPLICATION NUMBER: US 09/641,638
CURRENT FILING DATE: 2002-06-10
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 320
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens

FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 10-308-116 : polymorphic base C or T

FEATURE:
NAME/KEY: misc_binding
LOCATION: 481..500
OTHER INFORMATION: 10-308-116.mis1, potential

FEATURE:
NAME/KEY: misc_binding
LOCATION: 502..521
OTHER INFORMATION: 10-308-116.mis2, potential complement

FEATURE:
NAME/KEY: primer_bind
LOCATION: 386..403
OTHER INFORMATION: upstream amplification primer

FEATURE:
NAME/KEY: primer_bind
LOCATION: 754..771
OTHER INFORMATION: downstream amplification primer, complement

FEATURE:
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 10-308-116 potential probe

US-10-170-097-320

Query Match 88.2%; Score 82; DB 3; Length 1001;
Best Local Similarity 98.9%; Pred. No. 3.2e-18;

Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60
DB 394 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 453
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAG 93
DB 454 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAG 487

RESULT 3

US-09-949-016-15685
Sequence 15685, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15685
LENGTH: 26103
TYPE: DNA
ORGANISM: Human

US-09-949-016-15685

Query Match 88.2%; Score 82; DB 3; Length 26103;

Best Local Similarity 98.9%; Pred. No. 6.8e-18;

Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 60
DB 1908 TGAGTGGACCCCGGTCGCCGGTGGGGAATTTCTTGGCTCTCTGCGAGCCTTGAATG 1967
QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGCGAG 93
DB 1968 CCAGGCTCAGCCCTCATCTCTCTCTCTGCGAG 2001

RESULT 4

US-09-949-016-11879
Sequence 11879, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED,
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11879
LENGTH: 26105
TYPE: DNA
ORGANISM: Human

US-09-949-016-11879

Query Match 88.2%; Score 82; DB 3; Length 1001;
Best Local Similarity 98.9%; Pred. No. 3.2e-18;

Query Match 88.2%; Score 82; DB 3; Length 26105;
Best Local Similarity 98.9%; Pred. No. 6.8e-18;
Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 TGAGTGCAGCCCGGTCGCCGCTGGGGAATTTCTTGGCTCTCTGGTGAGCCTTGAATG 60
Db 1910 TGAGTGCAGCCCGGTCGCCGCTGGGGAATTTCTTGGCTCTCTGGTGAGCCTTGAATG 1969
Qy 61 CCA-GCTCAGCCCTCATCTCTCTCTGAGG 93
Db 1970 CCAGGCTCAGCCCTCATCTCTCTCTGAGG 2003
RESULT 5
US-09-919-060-15
; Sequence 15, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-15
Query Match 99.4%; Score 36.6; DB 3; Length 1899;
Best Local Similarity 76.3%; Pred. No. 0.0089;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 26 GGAATTTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 84
Db 32 GGAACCTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 90
RESULT 6
US-09-919-060-16/c
; Sequence 16, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-16
Query Match 39.4%; Score 36.6; DB 3; Length 1899;
Best Local Similarity 76.3%; Pred. No. 0.0089;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 26 GGAATTTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 84
Db 1868 GGAACCTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 1810

RESULT 7
US-09-919-060-12
; Sequence 12, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Canis familiaris
; NAME/KEY: CD6
; LOCATION: (311..(1929)
; OTHER INFORMATION:
US-09-919-060-12
Query Match 39.4%; Score 36.6; DB 3; Length 2693;
Best Local Similarity 76.3%; Pred. No. 0.0096;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 26 GGAATTTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 84
Db 62 GGAACCTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 120
RESULT 8
US-09-919-060-14/c
; Sequence 14, Application US/09919060
; Patent No. 6638744
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Nancy
; APPLICANT: Brandt, Kevin S.
; TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
; FILE REFERENCE: AD-1
; CURRENT APPLICATION NUMBER: US/09/919,060
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/224,486
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-919-060-14
Query Match 39.4%; Score 36.6; DB 3; Length 2693;
Best Local Similarity 76.3%; Pred. No. 0.0096;
Matches 45; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 26 GGAATTTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 84
Db 2632 GGAACCTCTTGGCTCTCTGGTGAGCCTTGAATGCCAGCTCAGCCCTCATCTCTC 2574
RESULT 9
US-09-949-016-54781
; Sequence 54781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Db 4 ECDPGRWGIFLASWWSLEQSPSSLSAG 34
|||||

RESULT 3

US-10-260-937-63
; Sequence 63, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-937-63

Query Match 96.6%; Score 169; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 9.6e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ECDPGRWGIFLASWWSLEQSPSSLSA 30
|||||
DB 2 ECDPGRWGIFLASWWSLEQSPSSLSA 31
|||||

RESULT 4

US-10-260-937-14
; Sequence 14, Application US/10260937
; Publication No. US20030220306A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Daniel
; APPLICANT: Chandrasekharan, N. Vishvanath
; TITLE OF INVENTION: NOVEL CYCLOOXYGENASE VARIANTS AND
; FILE REFERENCE: 07913-007001
; CURRENT APPLICATION NUMBER: US/10/260,937
; CURRENT FILING DATE: 2002-09-28
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/326,133
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/373,225
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,575
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-260-937-14

Query Match 77.7%; Score 136; DB 4; Length 613;
Best Local Similarity 91.7%; Pred. No. 3.2e-09;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ECDPGRWGIFLASWWSLEQQLSP 24
|||||
DB 4 ECDPGRWGIFLASWWSLEQQAQP 27
|||||

RESULT 5

US-10-783-297A-6
; Sequence 6, Application US/10783297A
; Publication No. US20040235017A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Pharmaceutical Research and development
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF
; FILE REFERENCE: PRD-2041
; CURRENT APPLICATION NUMBER: US/10/783,297A
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-297A-6

Query Match 73.1%; Score 128; DB 5; Length 31;
Best Local Similarity 80.6%; Pred. No. 2.1e-09;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ECDPGRWGIFLASWWSLEQSPSSLSAG 31
|||||
DB 1 ECDPGRWGIFLASGGALNARLSPSSLSAG 31
|||||

RESULT 6

US-10-783-297A-11
; Sequence 11, Application US/10783297A
; Publication No. US20040235017A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson Pharmaceutical Research and development
; TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-3 AND USES THEREOF
; FILE REFERENCE: PRD-2041
; CURRENT APPLICATION NUMBER: US/10/783,297A
; CURRENT FILING DATE: 2004-02-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-297A-11

Query Match 73.1%; Score 128; DB 5; Length 630;
Best Local Similarity 80.6%; Pred. No. 3.7e-08;
Matches 25; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ECDPGRWGIFLASWWSLEQSPSSLSAG 31
|||||
DB 4 ECDPGRWGIFLASGGALNARLSPSSLSAG 34
|||||

RESULT 7

US-10-437-963-105915
; Sequence 105915, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 24, 2006, 11:03:01 ; Search time 1749 Seconds

(without alignments)
3022.551 Million cell updates/sec

Title: US-10-783-297A-3

Perfect score: 93

Sequence: 1 tgatcgagcccggtgcc.....tcattctctctctgcagg 93

Scoring table: IDENTITY_NUC

Gapop:10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_ov.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	93	100.0	93	6	CQ869567	Sequence
2	93	100.0	1238	8	HUMPROHSYN	L08404 Homo sapien
3	93	100.0	1893	6	CQ869572	Sequence
4	82	88.2	1001	6	AR582395	Sequence
5	82	88.2	26782	8	AF440204	Homo sapi
6	82	88.2	28670	8	AY449688	Homo sapi
7	82	88.2	199985	14	AL353767	Homo sapi
8	82	88.2	223020	8	AL162424	Human DNA
9	81	87.1	94	8	AY884200	Human
10	70	75.3	93	6	CQ869569	Sequence
11	70	75.3	1860	6	CQ869574	Sequence
12	44.8	48.2	10377	6	AX347123	Sequence
13	42	45.2	10377	6	AX347122	Sequence
14	38	40.9	38	6	CQ869578	Sequence
15	36.6	39.4	1899	6	AR411937	Sequence
16	36.6	39.4	1899	6	AR411938	Sequence
17	36.6	39.4	1901	4	AF535139	Canis fam
18	36.6	39.4	2693	6	AR411935	Sequence

C	19	36.6	39.4	2693	6	AR411936	Sequence
	20	36.6	39.4	2706	4	AF535138	Canis fam
	21	34.4	37.0	187858	9	AC153542	Mus muscu
C	22	32.8	35.3	210956	14	AC162366	Mus muscu
	23	32.8	35.3	258003	14	AC122205	Mus muscu
C	24	32.4	34.8	258484	14	AC125555	Rattus no
C	25	31.6	34.0	110000	14	CT005269_03	Continuation (4 of
C	26	31.4	33.8	100000	8	AP000077	Homo sapi
	27	31.4	33.8	156296	8	AP006206	Homo sapi
	28	31.4	33.8	157665	8	AP006205	Homo sapi
	29	31.4	33.8	170261	8	AC090809	Homo sapi
C	30	31	33.3	235097	14	AC159664	Bos tauru
	31	30.6	32.9	89936	15	AP004532	Lotus cor
	32	30.6	32.9	173588	8	AC116664	Papio ham
C	33	30.2	32.5	134156	8	AL357083	Human DNA
C	34	30.2	32.5	178145	8	AC018659	Homo sapi
C	35	30.2	32.5	224571	14	AC159850	Bos tauru
	36	30	32.3	1296	5	AF077092	Gallus ga
	37	30	32.3	1394	5	EX935055	Gallus ga
C	38	30	32.3	1802	5	AF076640	Gallus ga
C	39	30	32.3	143392	15	AC149299	Populus t
C	40	30	32.3	231140	14	AC098904	Rattus no
C	41	29.6	31.8	140031	14	AC121686	Rattus no
C	42	29.6	31.8	161179	14	AC066601	Homo sapi
C	43	29.6	31.8	171296	8	CNS06C86	Human chr
C	44	29.6	31.8	189332	14	AC155501	Zea mays
C	45	29.6	31.8	231198	14	AC126892	Rattus no

ALIGNMENTS

RESULT 1
LOCUS CQ869567 93 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 3 from Patent WO2004074311.
ACCESSION CQ869567
VERSION CQ869567.1 GI:51999447

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Qin, M., Flores, C., Zhang, S. P. and Codd, G. E.

TITLE Human cyclooxygenase-3 and uses thereof

JOURNAL Patent: WO 2004074311-A 3 02-SEP-2004;

JANSSEN PHARMACEUTICA N.V. (BB)

FEATURES Location/Qualifiers

source 1 93

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match	100.0%	Score 93	DB 6	Length 93
Best Local Similarity	100.0%	Pred. No. 1.3e-19	Indels 0	Gaps 0
Matches 93	Conservative 0	Mismatches 0		
Qy	1	TGAGTGGGACCCCGGTCGCGGAGGATTTCTTGGCCCTCTCGTGGAGCCTTGAATG	60	
Db	1	TGAGTGGGACCCCGGTCGCGGAGGATTTCTTGGCCCTCTCGTGGAGCCTTGAATG	60	
Qy	61	CCAGCTCAGCCCTCATCTCTCTCTCTGCGAGG	93	
Db	61	CCAGCTCAGCCCTCATCTCTCTCTCTGCGAGG	93	

RESULT 2

HUMPROHSYN

LOCUS

DEFINITION Homo sapiens prostaglandin H synthase 1 gene, complete promoter.

1238 bp DNA linear PRI 27-APR-1993

ACCESSION L08404
VERSION L08404.1 GI:190413
KEYWORDS prostaglandin H synthase 1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1238)
AUTHORS Wang, L.H., Hajibeigi, A., Xu, X.M., Loose-Mitchell, D. and Wu, K.K.
TITLE Characterization of the promoter of human prostaglandin H synthase-1 gene
JOURNAL Biochem. Biophys. Res. Commun. 190 (2), 406-411 (1993)
PUBMED 8427584
COMMENT Original source text: Homo sapiens (library: pWE15 cosmid genomic) male DNA.
FEATURES
 source
 1..1238
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /sex="male"
 /cell_type="lymphocyte"
 /tissue_lib="pWE15 cosmid genomic"
 899..1040
 promoter
 899..906
 intron
 1041..1133
 exon
 1134..1220
ORIGIN
 Query Match 100.0%; Score 93; DB 8; Length 1238;
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60
 DB 1042 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 1101
 QY 61 CCAGCTCAGCCCTCATCTCTCTCTCTCTGAGG 93
 DB 1102 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 1134
RESULT 3
LOCUS C0869572 1893 bp DNA linear PAT 13-SEP-2004
DEFINITION Sequence 8 from Patent WO2004074311.
ACCESSION C0869572
VERSION C0869572.1 GI:51999450
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Qin, N., Flores, C., Zhang, S.P. and Codd, G.E.
TITLE Human cyclooxygenase-3 and uses thereof
JOURNAL WO 2004074311-A 8 02-SEP-2004;
PATENT JANSSEN PHARMACEUTICA N.V. (BE)
FEATURES
 source
 1..1893
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
ORIGIN
 Query Match 100.0%; Score 93; DB 6; Length 1893;
 Best Local Similarity 100.0%; Pred. No. 1.2e-19;
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60

9 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 68
 QY 61 CCAGCTCAGCCCTCATCTCTCTCTCTCTGAGG 93
 DB 69 CCAGCTCAGCCCTCATCTCTCTCTCTCTGAGG 101
RESULT 4
LOCUS AR582395 1001 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 320 from patent US 6794143.
ACCESSION AR582395
VERSION AR582395.1 GI:56617764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1001)
AUTHORS Blumenfeld, M., Bougueleret, L., Chumakov, I. and Cohen, A.
TITLE Biallelic markers derived from genomic regions carrying genes involved in arachidonic acid metabolism
JOURNAL Patent: US 6794143-A 320 21-SEP-2004;
FRX Genset S.A.;
FEATURES
 source
 1..1001
 /organism="unknown"
 /mol_type="genomic DNA"
ORIGIN
 Query Match 88.2%; Score 82; DB 6; Length 1001;
 Best Local Similarity 98.9%; Pred. No. 4.9e-16;
 Matches 93; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 60
 DB 394 TGAGTGGACCCCGGTCGGGGAATTTCTTGGCTCTCTCTGAGCCTTGAATG 453
 QY 61 CCA-GCTCAGCCCTCATCTCTCTCTCTGAGG 93
 DB 454 CCAGCTCAGCCCTCATCTCTCTCTCTGAGG 487
RESULT 5
LOCUS AF440204 26782 bp DNA linear PRI 23-OCT-2002
DEFINITION Homo sapiens prostaglandin-endoperoxide synthase 1 (PTGS1) gene, exons 1 through 11 and complete cds.
ACCESSION AF440204
VERSION AF440204.1 GI:17017286
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 26782)
AUTHORS Scott, B.T., Haesttedt, S.J., Bovill, E.G., Callas, P.W., Valliere, J.E., Wang, L., Wu, K.K. and Long, G.L.
TITLE Characterization of the human prostaglandin H synthase 1 gene (PTGS1): exclusion by genetic linkage analysis as a second modifier gene in familial thrombosis
JOURNAL Blood Coagul. Fibrinolysis 13 (6), 519-531 (2002)
PUBMED 12192304
REFERENCE 2 (bases 1 to 26782)
AUTHORS Scott, B.T., Haesttedt, S.J., Bovill, E.G., Callas, P.W., Valliere, J.E., Wang, L., Wu, K.K. and Long, G.L.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2001) Pathology, University of Vermont, Burlington, VT 05403, USA
FEATURES
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 1..26782
 /organism="Homo sapiens"